

# FIG. 1A

10005549-102901

ctcgcctcctctcctacttggataactgtggtaattctagagctaatacatgccgacgggc 60  
gctgaccccccttcgcgggggggatgctgcatthtatcagatcaagaccaaccgggtcagc 120  
ccctctccggcccccgccggggggcgggcgccggcggtttggtgactctagataacctc 180  
gggccgatcgacgccccccgtggcgggcgacgaccattcgaacgtctgccctatcaact 240  
ttcgatggtagtcgccgtgcctaccatggtgaccacgggtgacggggaatcagggttcga 300  
ttccggagagggagcctgagaaacggctaccacatccaaggaaggcagcaggcgcgcaaa 360  
ttaccactcccggaggtggcgggcgccatcttggcgaaggggggatcaggaagtgcg 420  
gaccgcggcgggcgggcgggcgggcgggcgggcgggagcccgagcgcaggccggaggctc 480  
ccggcccgcggcccccgagcggagcggagcggaggatgcagcagccgcagccgcagggg 540  
cagcagcagccggggccggggcagcagctggggggccagggggcggcggggggccggg 600  
ggcgggccagggggggggcccgggggccggggccctgcctgaggcgagagctgaagctgctc 660  
gagtcctatctccaccgcggccacgagcgttccgcattgccagcgcctgcctggacgag 720  
ctgagctgcgagttcctgctggctggggccggagggggccggggcgggggccgcgcccga 780  
ccgcctctccccccacgggggtcggtgcctggggatcctgtccgcctccactgcaacatc 840  
acggagtcataccctgctgtgccccccatctggtcggtggagtctgatgaccctaacttg 900  
gctgctgtcttgagaggctggtggacataaagaaaggaataactctgctattgcagcat 960  
ctgaagaggatcatctccgacctgtgtaaactctataacctccctcagcatccagatgtg 1020  
gagatgctggatcaacccttgccagcagagcagtgccacacaggaagacgtgtcttcagaa 1080  
gatgaagatgaggagatgcctgaggacacagaagacttagatcactatgaaatgaaagag 1140  
gaagagccagctgagggcaagaaatctgaagatgatggcattggaaaagaaaacttggcc 1200  
atcctagagaaaattaaaaagaaccagaggcaagattacttaaatggtgcagtgtctggc 1260  
tcggtgcaggccactgaccggctgatgaaggagctcagggatataaccgatcacagagt 1320  
ttcaaaggcggaactatgcagtcgaactcgtgaatgacagctctgtatgattggaatgtc 1380  
aaactcctcaaagttgaccaggacagcgctttgcacaacgatctccagatcctcaaagag 1440

FIG. 1B

aaagaaggagccgacttcattctacttaacttttcctttaagataactttccctttgac 1500  
ccaccatttgtcaggggtgtgtctccagtcctctctggagggatgttctgggcggaggg 1560  
gccatctgcatggaacttctcaccaaacagggctggagcagtgccctactccatagagtca 1620  
gtgatcatgcagatcagtgccacactgggtgaaggggaaagcacgagtgagttggagcc 1680  
aacaaatctcaatacagtcctgacaagagcacagcagtcctacaagtccttggtgcagatc 1740  
cacgaaaaaaacggctggtacacacccccaaaagaagacggctaaccctggagtatcacc 1800  
cttcctccctccccaggcaccactggaccaattacctttgaatgctgtatttgatctca 1860  
cgctgcctctgtggttcctccctcatttttctggacgtgatagctctgcctattgcag 1920  
gacaatgatggctattctaaacgctaaggaaaaaaaacaaacacagaactgtttcaagta 1980  
ctcaagactgacttacagaccaaccaaccaccttgctggaacccttgctagcaggcattc 2040  
ttataaaagaaactttcgagcctccttatattgctggaaactcagctgtgctccagacta 2100  
gagcctccttacctatgctatggatttttaattttattttctcttatttcattgtactgc 2160  
tttttttggttacagtgtatgatggatgtgtatgaaaaaatgtatctttgggaaaacaa 2220  
ttacagtttggttaatttgaaaaaaaaaaaaaaaaa 2280

(SEQ ID NO:1)

1005549.102901

FIG. 2A

CTCGCTCCTCTCCTACTTGGATAACTGTGGTAATTCTAGAGCTAATACATGCCGACGGGC  
GCTGACCCCTTCGCGGGGGGGATGCGTGCAATTTATCAGATCAAGACCAACCCGGTCAGC  
CCCTCTCCGGCCCCCGGCCGGGGGGCGGGCGCCGGCGGCTTTGGTGAATCTAGATAACCTC  
GGGCCGATCGCACGCCCCCGTGGCGGCGACGACCATTCGAACGTCTGCCCTATCAACT  
TTCGATGGTAGTCGCGGTGCCTACCATGGTGACCACGGGTGACGGGGAATCAGGGTTCTGA  
TTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAA  
TTACCCACTCCCGAGGTGGCGGCGGCGCCATCTTGGCGAAGGGGGGATCAGGAAGTGCG  
GACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGCCCGAGCGCAGGCGGAGGCTC  
CCGGCCCCCGGCCCGGAGCGGAGCGGAGCGGAGGATGCAGCAGCCGAGCCGAGGGG  
M Q Q P Q P Q G  
CAGCAGCAGCCGGGGCCGGGGCAGCAGCTGGGGGGCCAGGGGGCGGCGCCGGGGCCGGG  
Q Q Q P G P G Q Q L G G Q G A A P G A G  
GGCGGCCCGGGGGGGGGCCCGGGGGCGGGGCCCTGCCTGAGGCGAGAGCTGAAGCTGCTC  
G G P G G G P G P G P C L R R E L K L L  
GAGTCCATCTTCCACCGCGGCCACGAGCGTTCCGCATTGCCAGCGCCTGCCTGGACGAG  
E S I F H R G H E R F R I A S A C L D E  
CTGAGCTGCGAGTTCTGCTGGCTGGGGCCGAGGGGGCCGGGGCGGGGGCCGCGCCCGGA  
L S C E F L L A G A G G A G A G A A P G  
CCGCATCTCCCCCACGGGGGTGGTGCTGGGGATCCTGTCCGCATCCACTGCAACATC  
P H L P P R G S V P G D P V R I H C N I  
ACGGAGTCATACCCTGCTGTGCCCCCATCTGGTGGTGGAGTCTGATGACCCTAACTTG  
T E S Y P A V P P I W S V E S D D P N L  
GCTGCTGTCTTGGAGAGGCTGGTGGACATAAAGAAAGGAATACTCTGCTATTGCAGCAT  
A A V L E R L V D I K K G N T L L L Q H  
CTGAAGAGGATCATCTCCGACCTGTGTAACTCTATAACCTCCCTCAGCATCCAGATGTG  
L K R I I S D L C K L Y N L P Q H P D V  
GAGATGCTGGATCAACCTTGCCAGCAGAGCAGTGCACACAGGAAGACGTGTCTTCAGAA  
E M L D Q P L P A E Q C T Q E D V S S E  
GATGAAGATGAGGAGATGCCTGAGGACACAGAAGACTTAGATCACTATGAAATGAAAGAG  
D E D E E M P E D T E D L D H Y E M K E  
GAAGAGCCAGCTGAGGGCAAGAAATCTGAAGATGATGGCATTGGAAGAAAGAACTTGGCC  
E E P A E G K K S E D D G I G K E N L A  
ATCCTAGAGAAAATTAAAAAGAACCAGAGGCAAGATTACTTAAATGGTGCAGTGTCTGGC  
I L E K I K K N Q R Q D Y L N G A V S G  
TCGGTGCAGGCCACTGACCGGTGATGAAGGAGCTCAGGGATATATACCGATCACAGAGT  
S V Q A T D R L M K E L R D I Y R S Q S  
TTCAAAGGCGGAACTATGCAGTCGAACTCGTGAATGACAGTCTGTATGATTGGAATGTC  
F K G G N Y A V E L V N D S L Y D W N V  
AAACTCCTCAAAGTTGACCAGGACAGCGCTTTGCACAACGATCTCCAGATCCTCAAAGAG  
K L L K V D Q D S A L H N D L Q I L K E  
AAAGAAGGAGCCGACTTCACTTAACTTTTCTTTTAAAGATAACTTTCCCTTTGAC  
K E G A D F I L L N F S F K D N F P F D  
CCACCATTTGTCAGGGTTGTGTCTCCAGTCTCTTGGAGGGTATGTTCTGGGCGGAGGG  
P P F V R V V S P V L S G G Y V L G G G  
GCCATCTGCATGGAACCTTCTACCAAACAGGGCTGGAGCAGTGCCTACTCCATAGAGTCA  
A I C M E L L T K Q G W S S A Y S I E S  
GTGATCATGCAGATCAGTGCCACACTGGTGAAGGGGAAAGCACGAGTGCAGTTTGGAGCC  
V I M Q I S A T L V K G K A R V Q F G A

1005549.102901

FIG. 2B

AACAAATCTCAATACAGTCTGACAAGAGCACAGCAGTCCTACAAGTCCTTGGTGCAGATC  
N K S Q Y S L T R A Q Q S Y K S L V Q I  
CACGAAAAAACGGCTGGTACACACCCCCAAAAGAAGACGGCTAACCCCTGGAGTATCACC  
H E K N G W Y T P P K E D G \*  
CTTCCTCCCTCCCCAGGCACCACTGGACCAATTACCTTTGAATGCTGTATTTGGATCTCA  
CGCTGCCTCTGTGGTTCCCTCCCTCATTTTTCCTGGACGTGATAGCTCTGCCTATTGCAG  
GACAATGATGGCTATTCTAAACGCTAAGGAAAAAAAACAAACACAGAACTGTTTCAAGTA  
CTCAAGACTGACTTACAGACCAACCAACCACCTTGCTGGAACCCCTTGCTAGCAGGCATTC  
TTATAAAAGAAACTTTTCGAGCCTCCTTATATTGCTGGAACTCAGCTGTGCTCCAGACTA  
GAGCCTCCTTACCTATGCTATGGATTTTAAATTTATTTTCTCTTATTTTCATGTACACTGC  
TTTTTTTGGTTACAGTGTATGATGGATGTGTATGAAAAAATGTATCTTTGGGAAAACAA  
TTACAGTTTGTTAATTTGAAAAAAAAAAAAAAAAA

1005549-102901

FIG. 3

MQQPQPQGQQ	QPGPGQQLGG	QGAAPGAGGG	PGGGPGPGPC	40
LRRELKLLS	IFHRGHERFR	IASACLDELS	CEFLAGAGG	80
AGAGAAPGPH	LPPRGSVPGD	PVRIHCNITE	SYPAVPPIWS	120
VESDDPNLAA	VLERLVDIKK	GNTLLLQHLK	RIISDLCKLY	160
NLPQHDPDEM	LDQPLPAEQC	TQEDVSSSEDE	DEEMPEDTED	200
LDHYEMKEEE	PAEGKKSEDD	GIGKENLAIL	EKIKKNQRQD	240
YLNGAVSGSV	QATDRMLKEL	RDIYRSQSFK	GGNYAVELVN	280
DSLVDWNVKL	LKVDQDSALH	NDLQILKEKE	GADFILLNFS	320
FKDNFPDPP	FVRVSPVLS	GGYVLGGGAI	CMELLTKQGW	360
SSAYSIESVI	MQISATLVKG	KARVQFGANK	SQYSLTRAQQ	400
SYKSLVQIHE	KNGWYTPPKE	DG		422

(SEQ ID NO:2)

1005549 102901  
T0620T " 645000T

FIG. 4

1 65

RATL1d6 (1) MQQPQPQGGQPGPGQQLGGQGAAPGAGGGPGGGPGPGPCLRRELKLLSIFHRGHIERFRIASAC

T21349\_F25H2.8\_Cel (1) -----MACLRKLKEDIQVLEKLFKPNHNRFOILSAS

AAF45767\_EG:25E8\_Dr (1) -----MACLNTLKQEIKTLEKIFKPNHERFOILNSS

66 130

RATL1d6 (66) LDELSCBELLAGAGGAGAGAAPGPHLPPRGSVPGDPVRIHCNITTESYPAPVPIWSVESDDPNLAA

T21349\_F25H2.8\_Cel (32) VDELSMKFINAEN-----KG-----IIVTANIQENYPROPPPIWFSESDDVPVIG

AAF45767\_EG:25E8\_Dr (32) VDELLCRFIDKNG-----KR-----YDIHANITETIYESSPPVWFAESEETSVTN

131 195

RATL1d6 (131) VLERLVDIKKNTLLQLHLKRIISDLCKLYNLPHQPDVEMLDQPL-----

T21349\_F25H2.8\_Cel (76) MSLQRLTETEESTNLIHQVHRLVSDLCSEFYNLQMPCELPQIAPFVRDD-----IDEGRGSDI

AAF45767\_EG:25E8\_Dr (76) AVQILSNTNGRDNHVINQVIGILLRELCLRLHNVLPPDIDNLALPLQTPPPSASPLRCEQRPGGGG

196 260

RATL1d6 (176) -----PAEQCTQEDVSSSEDEDEEMPEDTEDLDHYEMKEEPAEGKKSSEDDGIGKENLAIDEKIK

T21349\_F25H2.8\_Cel (133) SDTTSEPIDDDMAGDGEVDDDEEEEDDEDADGDIIEIVEMAEDPTSQHDVGVSKEGUDMLDKVS

AAF45767\_EG:25E8\_Dr (141) AGGGGGPHGNEETSDSQEEIEDPIGESEGESEGEDDLPLEMDDDRSTSKDDMEVHATIEKLR

P52483\_UB6B\_MOUSE (1) -----MSSDRQSRSDDESPTSSGSSDADQRPD

261 325

RATL1d6 (235) KNORQDYLNQAVSGSVQATDRLMKELRDIYRSQSFKGGNYAVELVN-DSLYDWNVKKLKVQDSA

T21349\_F25H2.8\_Cel (198) KINRQOHLDDGKVOGSITATDRLMKELIRDIHRSEHFKNIGIYTFELEKEENLYQWIKLHKVDEDS

AAF45767\_EG:25E8\_Dr (206) QSQRQDYLNKSGSVQATDRLMKELRDIYRSQSFKGGNYAVELVN-ESIYEWNIIRLKSVDPDSP

P52483\_UB6B\_MOUSE (28) AAPKPEEQEERKPSATQOKKNTKLSSKITAKLSTSAKRIQKELAEITLDPNPNCSAGPKGDNIE

P27924\_UBC1\_HUMAN (1) -----MANIAVQRIKREFKEVLKSEETSKNQIKVDLVD-----ENFT-E

CAA72184\_UBCD4\_Dr (1) -----MANMAVSRIKREFKEVMRSEIIVQCSIKIELVN-----DSWTE

P14682\_UBC3\_YEAST (1) -----MSSRKSTASSILLROYRELTDPKKAIPSFHIELEDD-----SNIFTW

326 390

RATL1d6 (299) LHNDLQILKEKEGA-DFILLNFSFKDNFPDPPFVRVVSPLVSGGYVLGGAIICMELLTKQG---

T21349\_F25H2.8\_Cel (263) LFEDMKKLKKDHNQ-DHLLFSFTENEKFPDPPFVRVVAAPHINQGFVLGGAIICMELLTKQG---

AAF45767\_EG:25E8\_Dr (270) LHSDLQMLKEKEGK-DSILLNLFKEKTYPFEPFVRVVPPIISGGYVLGGAIICMELLTKQG---

P52483\_UB6B\_MOUSE (93) WRSTILGPPGSVYEGGVFFDDITFSSDYPEKPPKVTFRTRIYHCNINSQ-GVICLDILKDN----

P27924\_UBC1\_HUMAN (39) LRGETAGPPDTPYEGGKFLBETIKVPETYPFNPPKVRFITKIWHPNISSVTGAICLDILKDN----

CAA72184\_UBCD4\_Dr (39) LRGETAGPPDTPYEGGKFLBETIKVPETYPFNPPKVRFITKIWHPNISSVTGAICLDILKDN----

P14682\_UBC3\_YEAST (43) NIGVMVLNEDSIYHGGFFKAQMRFPEDFPSPQFRFTPAIYHPNVYRD-GRLCISILHQSGDPM

391 455

RATL1d6 (360) -----WSSAYSIESVIMQISATLVKKGKARVQFCANK-----SOYSLTRAQQSFKSLVQI

T21349\_F25H2.8\_Cel (324) -----WSSAYSIESCILQIAATLVKGRARISFDAKHT-----STYSMARAAQSFKSLQOI

AAF45767\_EG:25E8\_Dr (331) -----WSSAYTVEAVIMQIAATLVKKGKARIQFGATKALTQ-----GOYSLARAQSFKSLVQI

P52483\_UB6B\_MOUSE (153) -----WSPALTISKVLLSICSLLTDCNPADFLVGSIA-----OYLTNRAEHDRAROWT

P27924\_UBC1\_HUMAN (100) -----WAAAMTLRTVLLSLQALLAAAEPPDPCDAVVAN-----QYKQNPMPKQTARLWA

CAA72184\_UBCD4\_Dr (100) -----WAAAMTLRTVLLSLQALLAAAEPPDPCDAVVAY-----QFKDKYDLFLLTAKHWT

P14682\_UBC3\_YEAST (107) TDEPDAETWSPVQTVESVLSISVSLLEDPNINSEANVDAADVYRKNPEOYKQVRKMEVERSKODI

456 520

RATL1d6 (409) HEKNGWYTPPKEDG-----

T21349\_F25H2.8\_Cel (374) HAKSGCTFLCSTPSSHFFALHLVFFLHSDFFFNGLKSETFTFFKLSFRGYISSLVLYSFSRHL

AAF45767\_EG:25E8\_Dr (384) HEKNGWYTPPKEDG-----

P52483\_UB6B\_MOUSE (203) KRYAT-----

P27924\_UBC1\_HUMAN (150) HVYAGAFVSSPEYTKKIENLCAMGFDRNAVIVALSSKSWDVETATELLSN-----

CAA72184\_UBCD4\_Dr (150) NAYAGGPHTFPDCDSKIQRERDMGIDEHEARAVLSKENWNLEKATEGLFS-----

P14682\_UBC3\_YEAST (172) PKGFIMPISSEYISQSKLDEPESNKDMADNFWDSDLDDENGSVILQDDDYDDGNNHIPFEDD

521 579

T21349\_F25H2.8\_Cel (439) HHPFFTRFLIPQLQPPPIPFQLIPPFLNRTKHV-----

P14682\_UBC3\_YEAST (237) DVYNYNDNDDDDERIEFEDDDDDDDSIDNDSVMDRKQPKHAEDESEDVEDVERVSKKI

1000545-106201

# FIG. 5A

## RATL1d6 BLAST results/alignment w/ Drosophila protein

>GCGPROT:O46068 EG:25E8.2 PROTEIN.

Length = 394

Score = 369 bits (936), Expect = e-101

Identities = 194/403 (48%), Positives = 265/403 (65%), Gaps = 51/403 (12%)

Query: 41 LRRELKLLSIFHRGHERFRIASACLDLSCEFLLAGAGGAGAGAAPGPHLPPRGSVPGD 100  
L++E+K LE IF + HERF+I ++ +DEL C F+ .G

Sbjct: 7 LKQEIKTLEKIFPKNHERFQILNSSVDLLCRFI-----DKNGK 45

Query: 101 PVRIHCNITESYPVPPPIWSVESDDPNLAALVLERLVDIKKGNTLLQLHLKRIISDLCKLY 160  
IH NITE+YP+ PP+W ES++ ++ ++ L + + ++ + ++ +LC+L+

Sbjct: 46 RYDIHANITETYPSSPPVWFAESEETSVTNAVQILSNTNGRDNHVINQVGILLRELRLH 105

Query: 161 NLPQHDPDVEMLDQPLPAEQCTQEDVSSSEDE-----DEEMPEDTEDLDHYEM 206  
N+P PD++ L PL + + E +EE D E+++

Sbjct: 106 NVPLPPDIDNLALPLQTPPPSASPLRCEQRPGGGGAGGGGGPHGNEETDSDQEEIEDPIG 165

Query: 207 KEEPAEGKK-----SEDDGIGKENLAILEKIKKNQRQDYLNQAVSGSVQATD 254  
+ E+ +EG + S+ D + E+LA LEK++++QRQDYL G+VSGSVQATD

Sbjct: 166 ESEQESEGDEDLPLEMDDVRSTSKKDDMEVEHLATLEKLRSQRQDYLGKSVSGSVQATD 225

Query: 255 RLMKELRDIYRSQSFKGGNYAVELVNDSLYDWNVKLLKVDQDSALHNDLQILKEKEGADF 314  
RLMKELRDIYRS +FK Y++ELVN+S+Y+WN++L VD DS LH+DLQ+LKEKEG D

Sbjct: 226 RLMKELRDIYRSDAFKKNMYSIELVNESIYEWNIRLKSVDPSPLHSDLQMLKEKEGKDS 285

Query: 315 ILLNFSFKDNFPDPPFVRVSPVLSSGGYVLGGGAICMELLTKQGWSSAYSIESVIMQIS 374  
ILLN FK+ +PF+PPFVRV P++SGGYVL GGAICMELLTKQGWSSAY++E+VIMQI+

Sbjct: 286 ILLNLFKETYPPFPPFVRVHPIISGGYVLIGGAICMELLTKQGWSSAYTVEAVIMQIA 345

Query: 375 ATLVKGKARVQFGANKS----QYSLTRAQQSYKSLVQIHEKNG 413  
ATLVKGKAR+QFGA K+ QYSL RAQQS+KSLVQIHEKNG

Sbjct: 346 ATLVKGKARIQFGATKALTQGGYSLARAQQSFKSLVQIHEKNG 388

1000549-106201-6455000

# FIG. 5B

## RATL1d6 BLAST results/alignment w/ C. elegans protein

>GCGPROT:Q93571 F25H2.8 PROTEIN.

Length = 471

Score = 317 bits (805), Expect = 6e-86

Identities = 178/397 (44%), Positives = 247/397 (61%), Gaps = 49/397 (12%)

Query: 41 LRRELKLLLESIFHRGHERFRIASACLDCEFLLAGAGGAGAGAAPGPHLPGRGSVPGD 100  
L+ ++++LE +F + H RF+I SA +DELS +F+ A G

Sbjct: 7 LKEDIQVLEKLFPPKNHNRQILSASVDELSMKFINAENKG----- 46

Query: 101 PVRIHCNITESYPVPPPIWSVESDD-PNLA AVLRLVDIKKGNLTLQLHLKRIISDLCKL 159  
+ + NI E+YP PPIW ESDD P + L+RL + ++ +T +L + R++SDLC

Sbjct: 47 -IIVTANIQENYPRQPPIWFSESDVDPVIGMSLQRLTETEE-STNILHQVHRLVSDLCSE 104

Query: 160 YNL-----PQHPDVE-----MLDQPLPAEQCTQEDVSSSEDEDEEMPEDTE 199  
YNL P D++ +P+ + +V +DE+EE ED +

Sbjct: 105 YNLQMPCELPQIAPPVRDDIDEGRGSDISDTTSEPIDDDMAGDGEVDDDDDEEEEDDEDAD 164

Query: 200 -DL DHYEMKEEPEAEGKKSEDDGIGKENLAILEKIKKNQRQDYLN GAVSGSVQATDRLMK 258  
D++ EM EE+P D G+ KE L +L+K+ K RQ +L+G V GS+ ATDRLMK

Sbjct: 165 GDIEIVEMAEDPTS---QHDVGVSKEGLDMLDKVSKINRQQLDQKVGQSITATDRLMK 221

Query: 259 ELRDIYRSQSFKGGNYAVELVND-SLYDWNVKKLVKVDQDSALHNDLQILKEKEGADFILL 317  
E+RDI+RS+ FK G Y EL + +LY W +KL KVD+DS L D++ LK+ D +L

Sbjct: 222 EIRDIHRSEHFKNIGIYTFELEKEENLYQWWIKLHKVDEDSPLFEDMKKLKDHNDHLLF 281

Query: 318 NFSFKDNFPFDPFVRVVPVLGGGYVLGGGAICMELLTKQGWSSAYSIESVIMQISATL 377  
+F+F + FP DPPFVRVV+P ++ G+VLGGGAICMELLTKQGWSSAYSIES I+QI+ATL

Sbjct: 282 SFTFNEKFPCDPPFVRVVPAPHINQGFVLGGGAICMELLTKQGWSSAYSIESCILQIAATL 341

Query: 378 VKGKARVQFGA-NKSQYSLTRAQQSYKSLVQIHEKNG 413  
VKG+AR+ F A + S YS+ RAQQS+KSL QIH K+G

Sbjct: 342 VKGRARISFDAKHTSTYSMARAAQSFKSLQQIHAKSG 378

1000549102901



FIG. 6

